**Amendments to the Claims**:

This listing of claims will replace all prior versions, and listings, of claims in the application:

**Listing of Claims**:

**Claims 1 to 5. (canceled)**

**Claim 6. (currently amended)** A method of selecting the most potential candidate nucleotide sequences **[[of]]** for an analytical ~~oligo-nucleic~~ oligonucleic acid selected from the group consisting of a probe and a primer, for use in an analysis of a target nucleic acid, the method comprising:

(a1) entering a nucleotide sequence of a target nucleic acid to be analyzed ~~into~~ **[[a]]** ~~computer~~ and a genomic nucleotide sequence of an organism from which the target nucleic acid is derived, into a computer;

(a2) extracting all n unit sequences contained in the genomic nucleotide sequence, wherein n is an integer of 2 or more;

(a3) counting the number of each of the extracted n unit sequences from step (a2) having the same nucleotide sequence;

(b) calculating an occurrence frequency of each of the n unit sequences occurring on the genomic nucleotide sequence ~~of the target nucleic acid on the basis of~~ , as a ratio of the number of each of the n unit sequences to a value of $4^n$ which corresponds to all of the n unit sequences formed of n nucleotide sequences[[,]] ~~wherein n is an integer of 2 or more;~~

(c) ~~listing~~ extracting all candidate nucleotide sequences, the candidate nucleotide sequences having p number of nucleotides and which are present on the nucleotide sequences of the target nucleic acid, wherein p is an integer larger than n by m, and m is an integer of 1 or more;

(d) ~~listing~~ extracting all of the n unit sequences contained in each of the candidate nucleotide sequences, said n unit sequences being the same as that extracted in step (a2);

(e) calculating an occurrence frequency index of each of the candidate nucleotide sequences on the basis of the occurrence frequency of the n unit sequence calculated in step (b), by multiplying all the occurrence frequencies of all the n unit sequences contained in each candidate nucleotide sequence with each other, wherein [[a]] the lower the occurrence frequency

index ~~indicates~~ [[a]]is, the higher the specificity of the candidate nucleotide sequences to the target nucleic acid is;

(f) selecting, from the candidate nucleotide sequences ~~listed~~ extracted in step (c), the candidate nucleotide sequences each having a lower occurrence frequency index than a certain threshold value, thereby obtaining [[the]] potential candidate nucleotide sequences, [[the]] said certain threshold value being arbitrarily set so that the potential candidate nucleotide sequences are substantially fewer than the candidate nucleotide sequences obtained from step (c);

(g1) estimating the stability of the intramolecular secondary structure of the potential candidate nucleotide sequences from step (f) based on the nucleotide sequences thereof; and

(g2) selecting, from the potential candidate nucleotide sequences of step (f), the most potential candidate nucleotide sequences having such a low stability of [[a]] ~~molecular~~ an intramolecular secondary structure as determined in step (g1) which [[is]] would not ~~capable of forming~~ result in the nucleotide sequence forming a stable intramolecular secondary

structure, ~~and whereby~~ so that the most potential candidate nucleotide sequences are capable of readily hybridizing with the target nucleic acid under hybridization conditions **[[**are**]]** ~~selected~~.

**Claim 7. (original)** The method according to claim 6, wherein said n is 5, 6, or 7.

**Claims 8 to 10. (canceled)**

**Claim 11. (currently amended)** The method according to ~~any one of claims~~ claim 6**[[**, 7, 9**]]** ~~or~~ **[[**10**]]**, wherein all **[[**of**]]** the calculations involved in steps (a1) to **[[**(f)**]]** (g2) are sequentially performed by a computer.

**Claim 12. (currently amended)** The method according to ~~any one of claims~~ claim 6**[[**, 7, 9**]]** ~~or~~ **[[**10**]]**, wherein said ~~nucleotide sequence of an~~ analytical ~~oligo nucleic~~ oligonucleic acid is used as a primer in **[[**(i)**]]** a PCR method for ~~detecting a specific nucleotide sequence present in a nucleotide sequence of~~

~~a nucleic acid by using an enzyme reaction which requires hybridization reactions of a nucleic acid~~ amplifying the target nucleic acid, or **[[(ii)]]** ~~in a hybridization reaction of a nucleic acid employing~~ as a probe for detecting the target nucleic acid.

**Claim 13. (new)** A method of selecting the most potential candidate nucleotide sequences for an analytical oligonucleic acid selected from the group consisting of a probe and a primer used in an analysis of a target nucleic acid, the method comprising:

(a1) entering a nucleotide sequence of a target nucleic acid to be analyzed and a genomic nucleotide sequence of an organism from which the target nucleic acid is derived, into a computer;

(a2) extracting all n unit sequences contained in the genomic nucleotide sequence, wherein n is an integer of 2 or more;

(a3) counting the number of each of the extracted n unit sequences from step (a2) having the same nucleotide sequence;

(b) calculating an occurrence frequency of each of the n unit sequences occurring on the genomic nucleotide sequence, as a ratio of the number of each of the n unit sequences to a value of $4^n$ which corresponds to all of the n unit sequences formed of n nucleotide sequences;

(c) extracting all candidate nucleotide sequences, the candidate nucleotide sequences having p number of nucleotides and are present on the nucleotide sequences of the target nucleic acid, wherein p is an integer larger than n by m, and m is an integer of 1 or more;

(d) extracting all of the n unit sequences contained in each of the candidate nucleotide sequences, said n unit sequences being the same as that extracted in step (a2);

(e) calculating an occurrence frequency index of each of the candidate nucleotide sequences on the basis of the occurrence frequency of the n unit sequences calculated in the step (b), by multiplying all the occurrence frequencies of all the n unit sequences contained in each candidate nucleotide sequence with each other, wherein the lower the occurrence frequency index

is, the higher the specificity of the candidate nucleotide sequences to the target nucleic acid is;

(f) selecting, from the candidate nucleotide sequences extracted in the step (c), the candidate nucleotide sequences each having a lower occurrence frequency index than a certain threshold value, thereby obtaining potential candidate nucleotide sequences, said certain threshold value being arbitrarily set so that the potential candidate nucleotide sequences are substantially fewer than the candidate nucleotide sequences obtained from the step (c);

(g1) estimating the Tm of the potential candidate nucleotide sequences from step (f) based on the nucleotide sequences thereof; and

(g2) selecting, from the potential candidate nucleotide sequences of step (f), the most potential candidate nucleotide sequences having a Tm value as determined in step (g1) which falls within a predetermined range, so that when a plurality of the most potential candidate nucleotide sequences are used to analyze the target nucleic acid, the most potential candidate

nucleotide sequences hybridize with the target nucleic acid simultaneously at the same temperature.

**Claim 14. (new)** The method of claim 13, wherein all the calculations involved in steps (a1) to (g2) are sequentially performed by a computer.

**Claim 15. (new)** The method according to claim 13, wherein said analytical oligonucleic acid is used as a primer in a PCR method for amplifying the target nucleic acid, or as a probe for detecting the target nucleic acid.